AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1-25. (canceled).

26. (currently amended): A method of sequencing all or part of a target nucleic acid molecule, said method comprising ~~the steps of:~~

~~(A)~~ determining the sequence of a portion of said target nucleic acid molecule,~~;~~

~~(B) determining the position of said portion within said target nucleic acid molecule;~~

~~(C) combining the information obtained in steps (A) and (B) to obtain the sequence of all or part of said target nucleic acid molecule; and~~

~~wherein step (B) is carried out by identifying a label which is incorporated into or onto said portion of said target nucleic acid molecule and which indicates the position of said portion within said target nucleic acid molecule.~~

wherein the position of said portion within said target nucleic acid molecule is determined by identifying a label which is associated with said portion of the target nucleic acid molecule and which indicates the position of said portion within the target nucleic acid molecule,

wherein the sequence and position information obtained is combined in order to obtain the sequence of said target nucleic acid molecule,

wherein the label which indicates the position of said portion within the target nucleic acid molecule is not used to determine the sequence of said portion,

and wherein the portion which is sequenced has 2 or more bases.

27-28. (canceled).

29. (currently amended): The method as claimed in Claim 26, wherein the portion which is sequenced has 4 or more ~~nucleotide~~ bases and/or the position of said portion within said target nucleic acid molecule is determined with an accuracy of less than 1 kb.

30. (previously presented): The method as claimed in Claim 26, wherein said portion is sequenced by identifying magnifying tags associated with the target nucleic acid molecule, wherein said magnifying tags correspond to one or more bases of an adapter binding region or to one or more bases in proximity to an adapter binding region, wherein said adapter binding region binds an adapter molecule which comprises:

(i) one or more of said magnifying tags, or

(ii) a means for attaching one or more of said magnifying tags.

31. (previously presented): The method as claimed in Claim 26, wherein the sequence of the target nucleic acid molecule is determined by assessing the complementary of a portion of said target nucleic acid molecule by a process comprising the steps of:

(i) treating said target nucleic acid molecule so that at least a region of said target nucleic acid molecule is converted into a form suitable for binding a complementary probe,

wherein said complementary probe is bound to a solid support or said complementary probe carries a means for attaching to a solid support;

(ii) binding said complementary probe to at least a portion of said region suitable for binding a complementary probe;

(iii) optionally repeating steps (i) and (ii), with the *proviso* that said complementary probe binds to an adjacent or overlapping region of said target nucleic acid molecule relative to the region to which the complementary probe of the previous cycle bound; and

(iv) determining the sequence of said target nucleic acid molecule by identifying the complementary probe(s) to which said target nucleic acid molecule bound.

32. (previously presented): The method as claimed in Claim 31, wherein in step (i) said form is a single-stranded nucleic acid molecule.

33. (previously presented): The method as claimed in Claim 31, wherein in step (ii) said portion is 4 to 12 nucleotide bases in length.

34. (previously presented): The method as claimed in Claim 26, wherein a portion of said sequence is determined by identifying magnifying tags associated with the target nucleic acid molecule, wherein said magnifying tags correspond to one or more bases of an adapter binding region or to one or more bases in proximity to an adapter binding region, wherein said adapter binding region binds an adapter molecule which comprises:

(i) one or more of said magnifying tags, or

(ii) a means for attaching one or more of said magnifying tags; and

an adjacent or overlapping portion of said sequence is determined by a process comprising the steps of:

(i) treating said target nucleic acid molecule so that a region of said target nucleic acid molecule is converted into a form suitable for binding a complementary probe, wherein said complementary probe is bound to a solid support or said complementary probe carries a means for attaching to a solid support;

(ii) binding said complementary probe to at least a portion of said region suitable for binding a complementary probe;

(iii) optionally repeating steps (i) and (ii), with the *proviso* that said complementary probe binds to an adjacent or overlapping region of said target nucleic acid molecule relative to the region to which the complementary probe of the previous cycle bound; and

(iv) determining the sequence of said target nucleic acid molecule by identifying the complementary probe(s) to which said target nucleic acid molecule bound.

35. (previously presented): The method as claimed in Claim 26, wherein said method is performed on a sample comprising a heterogeneous mixture of target nucleic acid molecules.

36-39. (canceled).

40. (previously presented): The method as claimed in Claim 26, wherein said magnifying tags comprise a nucleic acid sequence of at least two nucleotide bases.

41. (new): The method as claimed in claim 26, wherein said label is or comprises a polynucleotide.

42. (new): A method of sequencing all or part of a target nucleic acid molecule, said method comprising determining the sequence of a portion of said nucleic acid molecule,

wherein the position of said portion within said nucleic acid molecule is determined by identifying a label which is associated with said portion of the nucleic acid molecule and which indicates the position of said portion within the target nucleic acid molecule,

wherein the sequence and position information obtained is combined in order to align the determined sequence within the target molecule,

wherein the label which indicates the position of said portion within the target molecule is not used to determine the sequence of said portion, and wherein the portion which is sequenced has 2 or more bases.